the rigid and highly cross-linked cell wall impedes the efficient breakdown of biomass into fermentable sugars. Developing sugarcane varieties with altered biomass composition is vital for improving the efficiency of enzymatically hydrolyzing cellulose into glucose. With the aim of identifying the major biomass components that influence cell wall recalcitrance, enzymatic hydrolysis efficiency was measured in pretreated leaf and culm tissues of sugarcane genotypes that varied in fiber composition. The strongest negative associations with hydrolysis efficiency were observed for acid-insoluble lignin content, syringyl to guaiacyl (S/G) ratio and xylan content while acid-soluble lignin had a strong positive influence indicating that these traits should be the key focus for genetic modification and breeding. To accelerate the development of new sugarcane varieties, the genes controlling S/G ratio were investigated by sequencing the transcriptome of genotypes that had contrasting values for the trait. Differential expression between these genotypes was observed in genes encoding enzymes in the phenylpropanoid biosynthesis pathway, dirigent proteins and a number of secondary cell wall transcription factors which may be important targets for modifying S/G ratio. Furthermore, several sequence variants associated with S/G ratio were identified which may be promising markers for use in marker-assisted selection to advance the development of sugarcane varieties with improved enzymatic hydrolysis efficiency.

W1024: Sugar Cane (ICSB)

Exploiting *Erianthus* Diversity to Enhance Sugarcane Cultivars

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Introgression of *Erianthus arundinaceus* into the SRA sugarcane-breeding program has been a goal for researchers for many years. The *Erianthus* genome was finally accessible to sugarcane breeders with the identification in 2005 of the first *Saccharum/Erianthus* fertile hybrids, developed in China. Today, *Saccharum/Erianthus* BC3 and BC4 clones are available in Australia, and *Erianthus*-sugarcane hybrids have been characterised by cytogenetics and investigated for their potential resistance against pachymetra root rot, sugarcane smut and nematodes. Some clones have shown potential as new sources of resistance for incorporation into the SRA breeding program. These hybrids were created from *Erianthus* clones indigenous to China and their reaction to the above diseases is unknown in Australian conditions. In Meringa we also have access to many *Erianthus* clones of Indonesian origin. Some of these *Erianthus* clones have previously shown immunity to pachymetra root rot. In the late 1990s, these Indonesian *Erianthus* clones were used in crossing but no fertile hybrids were ever produced due to an incompatibility between the *Saccharum* and the *Erianthus* genomes. We revisited this untapped source of resistance by utilising the fertile *Erianthus* hybrids derived from China to cross with the Indonesian *Erianthus* of known resistance to pachymetra root rot. Here we report on the early stage results of introgressing Indonesian *Erianthus* into the SRA breeding program.

W1025: Sweetpotato Genomics

Toward a Hexaploid Sweetpotato Pan-Genome

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Sweet potato, *Ipomoea batatas* (2n=6x=90), is among the most important food crops in the world and an extremely important food crop for subsistence farmers in sub-Saharan Africa. Despite its significant importance, currently knowledge of the genetic, molecular, and physiological basis of key agronomic traits in sweet potato is very limited, which has substantially constrained the improvement of sweet potato varieties across the world. The polyploidy (hexaploid) and highly heterozygous nature of the